Seven paradoxes of modern humanity genesis in the framework of traditional paradigm

Yu. I. Lobanovsky

Summary

Seven important and highly indicative paradoxes – contradictions associated with the genesis of modern humanity, which are insoluble within any version of the traditional description of this process, are examined in this work. It is shown that these seemingly paradoxical features of the process, in accordance with the concept presented in [1 – 3], become not only natural consequences of it, but also additional evidences that this is exactly how it happened.

Key words: *Pleistocene – Sapiens – Neanderthals – Denisovans – Archeology – Paleogenetics – Monocentricity – Polycentricity – Out of Africa*

I. Introduction

Dynamic process of a small sapient group evolution that left Africa about 130 ka BP was described from a standpoint of systems analysis in works [1 – 3]. And this process led them to turning into Homo sapiens sapiens – the only human species that began to dominate on the Earth. It was shown how, in course of this process, one branch of the sapiens captured enclave in Levant from Neanderthals, and the other settled in Asia, mainly in the Southeast. How, after the explosion of Toba stratovolcano 72 ka BP, almost all Asian sapiens died, with the exception of three small groups that survived this Catastrophe: in Khatlon valley among Pamir mountains in the north, on Timor island in the south, and also on Big Luzon island in the east, which gave the beginning of three types of sapiens – northern, southern and eastern, and subsequently – three original races: Caucasians, Melanoids and Mongoloids. Further, northerners and easterners (with a lag of ~ 20 kyr) settled depopulated territories in Asia, and southerners – lands of Sahul, where there were never humans before. After that, northerners have waged a victorious war in Europe, as a result of which Neanderthals disappeared forever, and survived a new, at least, all-European catastrophe – Archiflegreo stratovolcano explosion. Then they re-settled on depopulated lands of Europe and cold northeastern Asian territories (from which they were later driven out by newcomers from east), and in the south there was a meeting of easterners with southerners on the so-called Wallace line. A group of northerners at the same time invaded Africa, and gradually almost completely drove out the aboriginal archaic sapiens there, forming Negroid race.

All elements of this process, description of which was obtained through the use of a systemic analysis of available information, are fully consistent with archaeological, anthropological, paleogenetic, paleoclimatic, geological, physical and other data known to us. Moreover, in works [1 – 3] it was also stated that the described concept answers almost all questions about origin and ways of settlement of modern mankind and removes those contradictions and problems that are interested by scientific community related to the topic under consideration.

Using the example of seven principle problems of modern mankind genesis, which have turned into paradoxes due to impossibility of their solution within the existing traditional paradigm, based on non-systemic thinking, torn into separate, weakly connected meaning clusters, shows how they are solved on the basis of the proposed systemic concept.

II. The origin of modern humanity: mono- or polycentricity?

The most important issue of modern humanity genesis is the question of mono- or polycentricity of its origin, that is, whether it arose at one moment in one of the regions of our planet, or in several places and at different periods of time. Since the process of acquisition of morphological characteristics complex by hominins, which anthropologists may (or may not) recognize as features of modern humans, occurred gradually and nonlinearly, dates of this transition vary by different researchers in the range of at least 200 – 315 ka BP to 30 – 40 ka BP [4 – 6]. With such temporal uncertainty, naturally, there is also a spatial uncertainty, and the question itself of place of modern man origin, in essence, can completely lose its meaning. Nevertheless, supporters of the hypotheses of mono- and polycentric origin continue to argue, at least, for about a hundred years.

In recent decades, thanks to advances in biology and, especially, paleogenetics (genomics) and DNA genealogy, views of supporters of human monocentric origin began to dominate. Indeed, in accordance with modern scientific views, the multi-regional origin of a species in animal kingdom is almost impossible. Something like this can only happen as a result of interspecific hybridization of a significant part of closely related species populations. However, even such speciation is unknown in mammals – only isolated cases of partial hybridization have been identified [7 – 9].

The most recent paleogenetics and DNA genealogical studies clearly and quite unequivocally indicate the unity of origin of all modern mankind. More than a quarter of a century ago, an attempt was made to objectively assess the proximity (or remoteness) of human populations, using genetic variation in hypervariable loci (polymorphic microsatellites), which was previously used for individual identification and analysis of the relationship of modern humans. The so-called phylogenetic evolutionary tree of Homo sapiens sapiens species was built, which unambiguously demonstrated the sequential separation of various human populations from a single trunk [10]. Research in the field of DNA genealogy shows a qualitatively absolutely similar splitting of the original Y-haplogroups originating from a single center [11]. Of course, it is possible and necessary to clarify the times and the geographical zones of haplogroups appearance (especially since the opinion has already been expressed about the need to revise the mutation rates used in time calculations [12]), but at least a qualitative conclusion about the unity of modern humans origin, made on the basis of these data, cannot cause doubts.

Moreover, the study of "archaic fragments" of DNA in modern humans, which are interpreted as traces of ancestor’s partial hybridization with Neanderthals, shows that the total length of these fragments in the genomes of modern humans is about the same everywhere. So from this point of view, it turns out that a single ancestral group of all modern humans had some kind of contact with Neanderthals before they split first into separate populations, and then into races (Denisovan admixtures to human genome will be described in Section V of this article – when they are considered within the framework of standard paradigm, paradoxes also arise). In addition, it can be noted that any hybridization with earlier hominins ("erectoids" – various subspecies of Homo erectus) was not recorded in our ancestors [13].

At the same time, in works [14, 15], published a few years earlier, "A complex of facts was discovered, indicating the partial reproductive incompatibility of Neanderthals and Sapiens. Apparently, most of the introduced Neanderthal genetic material turned out to be not useful for the Sapiens, but harmful ... for several hundred millennia, during which the sapiens and Neanderthals lived in isolation in Africa and Eurasia, they were able to accumulate many incompatible alleles – "genes of speciation". This made it difficult for subsequent hybridization, making them actually different species (and not races or subspecies, as many anthropologists believed)" [16].

It’s hard to imagine that academician A. P. Derevianko – the oldest Russian archeologist, is not familiar with at least some of the evidences described above for the unity of modern mankind origin – because any of them is enough for an unambiguous conclusion. However, 10 years ago, he essentially revived F. Weidenreich's eighty-year-old hypothesis that Homo sapiens has included 4 subspecies of hominins (as Weidenreich pointed out): Homo sapiens africaniensis living in Africa about 200 ka BP, Homo sapiens Neanderthalensis in Europe up to 40 – 30 ka BP, in North and Central Asia until the same time – Homo sapiens altaensis, as well as unknown to us, but allegedly existed in Southeast and East Asia Homo sapiens orientalensis, which arose as a result of hybridization of sapiens with different "erectoids", that is, the last subspecies of Homo erectus which have survived there until recently [6, 17, 18].

It must be assumed that this obstinate adherence of academician to essentially marginal hypothesis is caused not simply by his stubbornness. Although the feeling that paleogenetic data clearly contradict his hypothesis leads A. P. Derevianko to attempts of interpretation any information in his favor, even not directly related to the case. For example, in 2018, commenting on really interesting data that "sequencing" ... DNA of a "Denisovan" girl from an Altai cave showed that her great-great-grandmother was a "Neanderthal", and her great-great-grandfather was a "Denisovan", said: "An article has been published, [which] finally confirmed the possibility of the hypothesis that modern humans were formed from these four subspecies" [19]. Thus, a single case of successful hybridization of individuals of two subspecies, or very closely related species – Neanderthals and Denisovans, completely usual for biology, became proof of wide continuous hybridization of sapiens with Neanderthals, Denisovans, and even erectus, which are much more biologically and genetically distant from them.

However, there are also objective, purely archaeological grounds for already at least 10 years of A. P. Derevianko disregard of all the arguments resulting from materials accumulated in biology, paleogenetics and DNA genealogy. He wrote: "The development of Paleolithic culture in East and Southeast Asia, including island world, proceeded in a fundamentally different way than in Africa and Western Eurasia. No external innovation in stone industries of the so-called Sino-Malay zone in the period 80 – 30 ka BP, which refutes the hypothesis of eastern part of Asia and Australia colonization by modern anatomical type human who came from Africa. Asian Homo erectus developed in East and Southeast Asia for over 1 million years. ... These data allow us to speak about a special model of Paleolithic industries development in East and Southeast Asia and about formation of a modern anatomical human, Homo sapiens orienthalensis, on the basis of local erectoid form of Homo. … Proposed [see above] designation of four subspecies and their unification into a single species Homo sapiens sapiens sensu lato will be completely unexpected for most colleagues, but this conclusion is based on large amount of accumulated archaeological data" [6].

There must be said that the opinion of the largest Russian archaeologist about low variability of stone industries in eastern part of Asia and in Australia before ~ 35 ka BP is undoubtedly fair, and it cannot be simply ignored, as practically all paleogeneticists do implicitly in their studies concerning migration of our ancestor's populations. As you know, in Europe, from about 45 ka BP in Neanderthals area, lost by their original owners at the same time, was happened what is commonly called Upper Paleolithic or Late Paleolithic revolution, or MSA/LSA transition, or "sudden replacement" of Middle Paleolithic industries by Upper Paleolithic industries" [20] (somewhat earlier, this also happened in Levant, see below). "As for those regions where there were no Neanderthals in the Late Paleolithic and where, therefore, there was no one to compete with settling Homo sapiens, then there is either no Upper Paleolithic at all (East and Southeast Asia, Australia), or it is represented only by late artefacts (Hindustan, most of North Asia)" [21].

Thus, a contradiction is outlined, or, if you will, a paradox arises: a straightforward interpretation of modern paleogenetic data unambiguously indicates that the origin of modern mankind is monocentric, and the same interpretation of archaeological data makes researchers studying regional stone industries of the late Pleistocene tend to be polycentric.

The concept of mono- and polycentric origin of modern mankind simultaneously (only from different points of view) will be expanded in the next section of this article, and here we will briefly explain the absence of "external innovations in the stone industries ... of Sino-Malay zone in the period 80 – 30 ka BP". The speech here is clearly about sapient stone industries. From a systemic analysis of sapiens' migrations in this zone, it follows that the first appearance of their advanced groups just dates back to about 80 ka BP. A few thousand years later, about 72 ka BP, there was an all-world Catastrophe – a grandiose explosion of Toba stratovolcano, located in the west of Sunda subcontinent (now Sumatra Island). Naturally, this Catastrophe most strongly affected the nearby "Sino-Malay zone", and after death of all living things in vast territories, while intelligent life glimmered on islands in extreme east of Sunda and southeast of it, any "innovations" of any type in this zone became fundamentally impossible until the time of 45 – 40 ka BP (although in enclaves on the aforementioned outskirts of Sunda, our ancestors clearly made very significant progress in navigation) [1 – 3]. In addition, on northwestern outskirts of "Sino-Malay zone" external innovations – artifacts of Bohunitsky type appeared nevertheless somewhat earlier than A. P. Derevianko indicates for this region, about 35 ka BP (for example, at Shuidungou site [22, 23]).

After returning to "Sino-Malay zone", first of life, and then of intelligent life, the repeated expansion of our eastern ancestors over unsettled, but once again fertile land did not require any new ("land", not "sea") skills and, therefore, no "Upper Paleolithic revolutions" in the stone industries (artifacts associated with "marine" innovations have not remained for obvious reasons). This revealed fundamental difference between development of this region and what was happening at the same time with northerners in Levant and in periglacial zone of Eurasia on front of war in Neanderthal homeland [1 – 3]. The southerners who settled Sahul and surrounding islands found them in a similar situation with easterners – and they had no rivals there, and they did not need significant innovations after landing on the mainland. Only "father of all" according to Heraclitus – a brutal war of destruction caused the Upper Paleolithic revolution in Middle East and Europe, waves from which slowly but surely spread throughout almost the entire oecumene, which was greatly facilitated by the next, at least, all-European catastrophe – the explosion of Archiflegreo stratovolcano about 39.3 ka BP. After that, European innovations of stone industry, together with their carriers, reached, for example, Boomplaas Cave in extreme south of Africa by about 33 – 32.5 ka BP [1 – 3], and extreme west of Africa – by 21 – 11 ka BP (see below). In this regard, one can recall well-known "law of challenge and response" by A. Toynbee [24].

Consequently, in a systemic analysis, there are no contradictions between "monocentric" paleogenomic data, as well as the results of DNA genealogy, and "polycentric" archaeological data, that is, the paradox that led to the revival of F. Weidenreich's hypothesis by academician Derevianko does not exist in reality, but only in speculative unsystemic constructions.

III. How many times did our direct ancestors (Homo sapiens) leave Africa?

So, despite the heroic attempts of academician Derevianko on archaeological grounds to resurrect F. Weidenreich's hypothesis about the polycentric origin of modern mankind, heavy tread of modern paleogeneticists and representatives of DNA genealogy, erasing all alternatives, proves the genetic unity of modern human ancestors with splitting into modern haplogroups (genera) not earlier than 160 – 200 ka BP [11]. At this time, sapiens lived only in Africa, so at least one of their exits from Africa to Eurasia and Sahul was necessary. This raises the question, how many of these exits from Africa were there in reality, and where did they take place? And this is where the curious phenomenon of "flickering of genomic data" appears: over the past 10 years, as more and more paleogenetic results are obtained, ideas about number of successful exits of sapiens from Africa to Asia periodically change from one to two or more and again to one to then return to the previous ideas. Literally every high-profile article or group of articles on this topic turns the underlying trend from head to foot and back.

It looks quite comical, in principle, especially in perfectly written reviews of such articles in Russian on network resource “Elements. Science News". The fact is that all these reviews were written by the same person – a very qualified biologist, A. Markov, briefly and very clearly outlining the essence of these works. And this brevity and clarity, when these papers were presented by the same person, especially vividly demonstrate such trend reversals on average every 3 – 4 years, or even more often.

Let's start in 2011. A. Markov's review [25], including work [26] on the southern route of sapiens settlement from Africa, says: "Many experts suppose that modern non-African humanity has originated from not that population which enters to Asia through Nile corridor about 120 thousand years ago, but from another group of emigrants from Africa, who left their homeland by the "southern route", that is, crossed Bab al-Mandeb Strait to South Arabia and then settled along the coast of Indian Ocean to the east. ... The chronology of this second exodus from Africa remains controversial and relies mainly on indirect evidence. Some experts believe that it took place about 85 thousand years ago, and soon after that sapiens reached Indonesia and southern China". Thus, in 2011, the trend was the recognition of two exits of sapiens from Africa: about 120 ka BP through Sinai Peninsula, and sometime much later – through Arabia.

Five years later, in 2016, the article [27] was published on genomic studies of indigenous population of New Guinea and Australia. It explicitly and deliberately compared "well-founded hypothesis of one out-of-Africa event (1 OoA)", which assumes "that Neanderthal admixture presenting in genomes of Europeans, Asians and Australians has a single origin ... and ... second version two out-of-Africa events, (2 OoA) … supported by some archaeologists and geneticists" [28]. And there was written also that, according to version 2 OoA "ancestors of Papuans and Australians left Africa earlier than the rest". However, studies described in this article have shown that "Neanderthal admixture in genomes of Papuans and Australians clearly has the same origin as Neanderthal DNA inherited by Europeans and Asians". It follows that the ancestors of Papuans and Australians first met Neanderthals together with the ancestors of Europeans and Asians, and only after that separated from them. "If we take this circumstance into account and make appropriate amendments, it turns out that a more likely scenario is still one-time exit from Africa (1 OoA)" [28]. So, there was trend in 2016 – out of Africa was one.

However, already in 2017 there were even much more than two outputs [29]. "Comparative genomics data strongly indicate one episode of the exit from Africa, which took place about 60 ka BP. ... However, the available facts cannot be reduced to a simple model of a one-time exit from Africa. Too much data has accumulated indicating the presence of sapiens in various parts of Asia long before the 60,000-year-old mark. ... In general, the data available to date are in the best agreement with the multiple ancient (more than 60 ka BP) migrations of sapiens outside Africa, which left few traces in modern genomes (most likely, small groups left), and a single large migration of about 60 ka BP, which made main contribution to gene pool of current non-African humanity" [30].

We note right away that gene pool of "non-African and African humanity" (not counting small relict groups such as Khoisans or Pygmies) is, according to latest data, common, bearing the same "Neanderthal impurities" [31], see section IV of this article below. And within the framework of our specific question, it can be stated that according to article [29], there are many exits from Africa.

Thus, this very first careful attempt in the analysis to go a little beyond purely genetic information immediately breaks the previous trend and leads to conclusion that there was more than one exit from Africa, most likely a lot. True, in this work there was no slightest attempt to find out if this is possible, at least in principle, due to the existing natural and climatic restrictions on ability of hominins to cross the extremely deserts separating Africa and Asia under Ice Age conditions?

And finally, in 2021, in review article [32], a large group of scientists finally came to a consensus: "Genetic and archaeological data obtained in recent years, including data on the distribution of Neanderthal and Denisovan impurities in sapient genomes, confidently confirm the scenario of the recent (60 – 50 ka BP) exit from Africa of the sapiens group, which subsequently populated the whole world" [33]. But at the same time, there were an unknown number of other outputs that were not fixed by genetic methods. "The genetic data, however, clearly show that all these early emigrants from Africa either left no traces at all in modern gene pools, or these traces are insignificant" [33] (although, as the analysis carried out in section V of this work shows, traces in Neanderthals genome they once left). In addition, the time of this "main exit from Africa" became at least 1.5 times closer to us as earlier. It has changed, approximately, "from 85 ka BP" [26], "to 60 – 50 ka BPs" [32].

So the conclusion is this: science does not know whether there were "additional" outputs, and if there were, then why they did not leave traces, if they were. Although, in fact, there are actually many archaeological traces of earlier presence of sapiens in Eurasia [1], including traces imprinted in fossilized silt of Alathar paleolake in modern Nefud desert in the very literal sense of the word – traces of their feet dated about 121 – 112 ka BP [34]. And no exit of any hominins from Africa would have been possible 50 ka BP because of the drying out of deserts due to increasing cooling of climate at this time of the Ice Age [35]. However, it is quite possible to agree that "genetic and archaeological data ... confidently confirm the scenario" regarding the relatively recent (65 – 50 ka BP) output of sapiens, but where did it come from? All subclades that arose as a result of four deepest branching of the oldest Y-haplogroups DE and CF, except for one, gave rise to all existing haplogroups from C and E to Q, T and R, are non-African, and when describing the place of their origin at this time, it is indicated usually Central Asia and its environs [11]. In addition, how the representatives of this group of sapiens, according to article [32] "escaped 60" and, even more so, "50 ka BP from Africa", did they turn out at the same time to 55 ka BP in Manot Cave near western coast of Mediterranean Sea and on Lake Mungo in very distant South-East Australia [1 – 3]? So the treatment of the problem proposed in this article turns out to be worse than the disease itself – the conclusions become simply absurd.

The analysis of these problems allows us to conclude that all these fluctuations in results with an actual loss of their stability and with going beyond the reasonable limits are not accidental, but due to objective reasons. In this case, mathematician will say that such instability of the solution to the problem he is considering is caused by the fact that the problem is posed incorrectly. Translated into the language of humanities sciences, this means that wording "The exit of sapiens from Africa during the expansion of Eurasia and Sahul" is so narrow that it does not allow obtaining results that, in principle, could be consistent with the data of archeology, genomics, DNA genealogy, climatology, geology and physics of explosion. Therefore, the correct formulation of the problem should not bear numerical, geographical and time constraints of the exit locations leading to the instability of its solution, but should be formulated as follows: "The number of exits of sapiens is not a priori deterministic and is determined only during solution of the problem itself together with the identification of place and time each of them". The place of origin of sapiens, our ancestors, is undoubtedly Southeast Africa, which is uniquely determined by the currently available complex of established archaeological and genetic data. But in addition to the emergence of new species and populations in hominins, their disappearance also occurs, and in some cases – the passage through the so-called "bottlenecks" with a sharp drop in numbers during the crisis. And the number of these places of survival, preservation and new ascent and their geographic location are determined already in process of solving the problem (if there is enough available data for this, and the problem can be solved), and not postulated before the analysis of this process begins.

One has only to state the formulation of this problem, as all the facts are easily lined up in a single spatio-temporal sequence, described in the introduction: initially, a group of sapiens left Africa, met with Neanderthals, then divided into several populations. Later, most of them perished in the outbreak of global Catastrophe, and only three small groups – northerners, easterners and southerners – survived in three geographically isolated refugia enclaves – in foothills of Pamir and on South Asian islands [1 – 3]. It is this moment that qualitatively separates one sapiens era from another, it is natural to take as a starting point for beginning of the existence of modern mankind, since, as far as we know, this was the only qualitative leap (gap) on the more or less smooth trajectory of early African sapiens transformation into the species Homo sapiens sapiens, that is, in modern humans. And already the post-catastrophic expansion of our ancestors in depopulated Asia, previously uninhabited Sahul, Neanderthal Europe and Africa from three refugia-ancestral homelands consistently describes the features of all the processes that took place with them further [1 – 3]. Thus, in a strict (narrow) formulation, there were no exits of modern humans from Africa at all – they arose in three points of Asia after the catastrophic eruption of Toba stratovolcano from the sapiens that left Africa 60 – 55 kyr before that. And with any number of supposed exits of sapiens – our ancestors directly and exclusively from Africa, any variant of modern humanity genesis does not allow us to link together the entire complex of information we now have.

So there was only one successful exit of sapiens from Africa, and not modern humans themselves came out of there, but only their ancestors. Modern humanity is biologically and genetically one, but at the same time polycentric, since it emerged after the world Catastrophe from three Asian refugia-ancestral homelands, thus forming three original races: Caucasians (European), Mongoloids (Asians) and Melanoids (Australian aborigines, Papuans and Melanesians).

IV. How many times have our direct ancestors (Homo sapiens sapiens) entered Africa?

The next paradox, which has been observed for about 12 years and remains in public consciousness at the present time, is that it has become generally accepted that the famous paleogeneticist Svante Pääbo and his colleagues proved that inhabitants of Africa did not interbreed with Neanderthals, and in their genome has absolutely no traces of DNA of these aborigines of Eurasia, which are in genes of all other inhabitants of the Earth. And this became not just an opinion, but also a guide, directly and immediately applied in the construction of genomic analysis techniques. An example is the statement of one of paper [36] authors, where he said: "We know that contemporary non-Africans have traces of Neanderthal in them, so they were not useful in this search. Instead, we used the genomes of contemporary individuals … across Africa to identify mutations…" in genome of Eastern Neanderthal from Altai Denisova Cave, to search for an admixture of sapiens' genome, "pure" from Neanderthals (see [37]).

Moreover, this idea still continues to remain not only on pages of many media, but also in minds of some modern geneticists, which affects their methods of work, and, therefore, their results. The most recent example is a January 2022 publication [38] by 13 co-authors on a study of "OAS1/2/3 cluster" which "has been identified as a risk locus for severe COVID-19 among individuals of European ancestry, with a protective haplotype ... derived from Neanderthals". As the authors of this paper report: "This haplotype contains a splice variant of OAS1, which occurs in people of African ancestry independently of gene flow from Neanderthals", and Africans cannot have this protective variant of haplotype. They then repeat now debunked assertion "that the Neanderthal haplotype is virtually absent among individuals of primarily African ancestry", albeit with careful use of the words "predominantly" and "practically", which essentially eliminate the possibility of it falsification, thus deducing this assertion beyond the limits of scientific knowledge method. Wherein they even refer to article [31], in which Neanderthal genomic impurities in Africans were found and described. They write further: "… such variants [of risk locus] have existed in modern humans on the order of approximately half a million years and therefore co-segregate with different variants than when they are derived from gene flow from Neanderthals into modern humans that occurred about 60,000 years ago", using data of Pääbo with co-authors paper published ten years ago. Although, as was shown at least 6 years ago, the only significant "gene flow from Neanderthals" happened about 40 kyr earlier (see [36]). It must be assumed that all this not quite adequate historical picture of modern humanity genesis may influence the results of risk loci analysis on extremely hot modern front in the fight against the COVID-19 epidemic.

This opinion arose shortly after publication of a truly outstanding work – complete sequencing of Neanderthals genome in 2009, carried out by group of scientists led by Svante Pääbo and David Reich [39]. "Neanderthals are slightly more similar in their genome to people outside of Africa ", Pääbo said in an interview [40] (2010). At the same time, Reich said about Neanderthals that "It's a small but very real proportion of ancestry in non-Africans..." That is, both of them firmly ruled out the presence of Neanderthal gene impurities in the genome of modern Africans. Together with the results of analysis carried out in previous section of this work, this means that paleogenetics, in discussions about exodus of sapiens from Africa, did not notice the problem of isolating this continent from Eurasia due to natural and climatic conditions of the Ice Age, and, at the same time, were confident in the absolute isolation of Eurasia from Africa, even in interglacial period. It is difficult to imagine how both of these diametrically opposed thoughts could fit in one head, except if we assume that North African and Arabian deserts had properties of diodes, capable of conducting streams of sapiens in only one direction.

At the same time, it is known that the overwhelming majority of representatives of modern Negro race Y-haplogroups are the same as those of inhabitants of Eurasia, for example, main haplogroup E, which is extremely widespread in Africa among people of Negro race, according to the latest data, originated outside Africa [41]. And human contacts between these continents, at least in the Holocene, were obvious. Therefore, how Neanderthal genes could not be in Africa is difficult to understand. And finally, in 2020, article [31] was published, in which these genomic impurities were finally found and described. Its authors stated: "Strikingly, we find that African individuals carry a stronger signal of Neanderthal ancestry than previously thought". In fact, the only striking thing is that this caused at least some surprise among paleogeneticists. The explanation why this was not found earlier comes down to the fact that earlier the "reference assemblies" of African genotypes were incorrectly selected to identify Neanderthal traces in their genomes, and new method used in the work [31] does not use such "assemblies".

This case shows that new and not always properly worked out paleogenetic methods may well give incorrect results, so that a thoughtless and uncritical attitude towards them will always lead to next chain of delusions not only of geneticists, but also of anthropologists and archaeologists.

And in this particular case, the result of Pääbo and Reich seemed to close the possibility of sapiens entry into Africa from Eurasia after contact with Neanderthals. Fortunately, we immediately considered it as mistake, and according to archaeological data, we described the invasion of Africa from Europe by Cro-Magnons (Grimaldi) of about 36 ka BP (after all-European catastrophe of 39.3 ka BP), mainly replacing aboriginal African population [1 – 3]. It should be noted that the structure of the main African haplogroup E and the spatial distribution of its main subclades clearly indicate that after the entry of Grimaldi into Africa, this continent was again isolated from Eurasia for a long time (before the Holocene), which fully corresponds to that described in [1 – 3] concepts.

Thus, in the late Pleistocene, our direct ancestors entered Africa at least once, and as a result of this invasion, its population and genetic maps were completely redrawn.

V. Paradoxical Neanderthal and Denisovan admixtures to sapiens' genome and sapient admixtures to Neanderthal's genome

Paradoxes associated with properties of Neanderthal and Denisovan admixtures to genome of modern humans, which can be called dispersed, that is, associated with the pattern of their scattering over the Earth, have not yet been clearly formulated by scientific community due to the fact that a more or less indicative array of information about these characteristics of sapiens genome was formed literally very recently. However, objectively, they exist and can be clearly described.

As is known, in accordance with works on genomics, the distribution of Neanderthal impurities in the sapiens genome is very simple: all modern humans [13, 42], including Africans, have these impurities, but their number varies, reaching a maximum of about 2 % [31]. At the same time, "The low diversity among the Neanderthal haplotypes segregating in present-day populations indicates that, while more than one Neanderthal individual must have contributed genetic material to modern humans, there was likely only one major episode of admixture" [42], and this happened about 100 ka BP [36]. This means that contacts, which left a noticeable genetic trace, between modern sapiens and Neanderthals occurred only once and long before sapiens colonized Europe.

At first glance, this seems rather strange. According to any model of sapiens dispersal, they closely converged with Neanderthals at least 4 – 5 times. According to our concept (see below Fig. 1) – first in the Zagros Mountains or Iranian Highlands during movement of sapiens eastward to India in the range of 120 – 95 ka BP. Then, in Levant, western population of sapiens, which broke away from main group, fought for a place under the Sun with Neanderthals, in the period from about 110 – 105 ka BP to 72 – 70 ka BP, until after the Catastrophe disappeared there their traces completely.

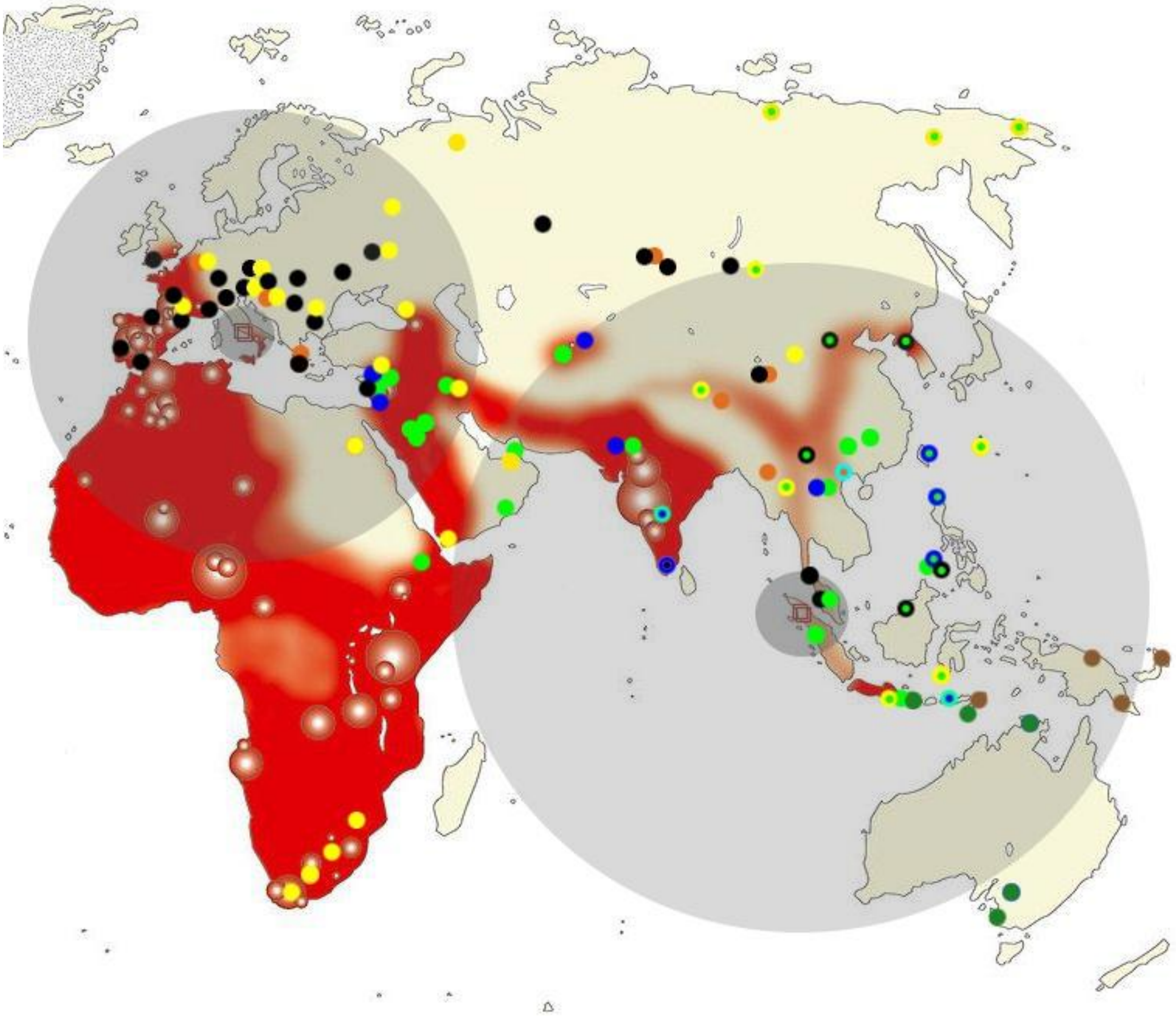

Fig. 1 – Places of considered Pleistocene sites and zones of catastrophic eruptions impact of two volcanoes against the background of Acheulean findings distribution

Gray circles are approximate zones of damage by shock waves during explosions of Toba (72 ka BP) and Archiflegreo (39.3 ka BP) stratovolcanoes, internal with a border of 10 kPa, external – 1 kPa, see [1 – 3]. Light green dots describe sites of sapiens in the period 130 – 72 ka BP; blue dots – 72 – 47.5 ka BP for northerners and easterners (for the latter – with a central light green dot), and for southerners – dark green dots. Black dots correspond to the period of 47.5 – 39.3 ka BP for northerners and easterners (as well as for the latter – with a central light green dot), and for southerners – dark brown dots. Yellow dots – period 39.3 – 30 ka BP. Dots of other colors refer to non-sapient hominin species.

Further – a new "interaction" with Neanderthals in Levant in the range from 55 to 48 – 47 ka BP [1 – 3], which, according to archaeological data from Boker Tachtit Cave in Negev desert (the southernmost blue point in Fig. 1 among cluster of multicolored "Levantine" points) in the period of initial Upper Pleistocene (IUP) 50 – 48 ka BP grew into "a cultural leap" [43] or, which is the same, into "Upper Paleolithic revolution", and, naturally, earlier than in Europe. This time, the "interaction" ended with the disappearance of Neanderthals without a trace forever. After that, sapient "steamroller" of Upper Paleolithic revolution rolled across all periglacial Europe 45 – 41 ka BP, and Neanderthals ended forever and there. There was another, apparently already less significant episode of contacts again in Zagros about 37 – 35 ka BP, when the last remnants of Neanderthals were killed, possibly descendants of those Levantines who succeed to escape alive after the defeat of 48 – 47 ka BP. And of all these episodes, only the first remained in genome of modern humans – the passage through Zagros and Iranian Highlands during movement of sapiens to the east.

"In contrast, Denisovan haplotype diversity reflects a more complex history involving more than one episode of admixture", see [42]. Indeed, it is already well known that Denisovan haplotypes are absent in Caucasians – descendants of northerners, but in Mongoloids – descendants of easterners and, especially, in Melanoids – descendants of southerners, their admixtures are found, at least not to a lesser extent than the Neanderthal ones [13, 27, 42, 44]. At the same time, Denisovan haplotypes exist in at least three lines: D0, D1 and D2, apparently corresponding to three significant contacts of sapiens with Denisovans, and D0 line (Denisovans from Altai) is traced among the inhabitants of East Asia, peoples of Siberia and American Indian tribes. Modern aborigines of Australia and Papuans of New Guinea retain traces of the D1 and D2 lines. In addition, D2 line is also available for residents of East Asia and Oceania. It was determined that D1 line separated from D0 line about 365 ka BP, and D2 line – about 285 ka BP [45].

As you know, Denisovans are sister group of Neanderthals, and their evolutionary divergence occurred about 640 ka BP [46]. Main area of Neanderthals settlement was periglacial mammoth steppe and, usually, mountainous and foothill regions to the south. The excavated sites of Denisovans also belong to cold climatic zones: Denisova Cave lies in Altai [18] (a pair of dark orange and black dots west of Lake Baikal in Fig. 1), and Altai at that time was covered with a glacier. Baishiya Cave is further to south, however, at ~ 3.3 km above sea level [47] (the same pair of points in Fig. 1 on the eastern outskirts of Tibet within a light red V-shaped fill describing the distribution of Acheulean findings). So it was a very cold-loving hominin species, usually settling near glaciers, where there was water, and, therefore, to think that it reached Sahul and nearby tropical islands, as some paleogenetics suggest to explain the presence of D1 Denisovan admixture, available only behind the Wallace Line and only in Australia, in the east of New Guinea and in New Ireland [13], it would be rather reckless (compare this zone with the location of dark green and dark brown dots in Fig. 1, that is, with the range resettlement of southerners). Neanderthals that are closed to Denisovans never appeared south of Levant, even in the Interglacial period, when deserts became passable.

Thus, first of four paradoxes formulated in this section of the article is a contradiction between a significant number of contacts between Neanderthals and northerners (and their ancestors), and low diversity of Neanderthal haplotypes in their descendants – Caucasians, and a significantly greater diversity of Denisovan haplotypes in genome of Asians and Melanoids with relatively small number of contacts of their ancestors with Denisovans. Indeed, now only 2 sites of Denisovans are known, described in the paragraph above, and there are two more highly probable such points – Quesang in the south of Tibet [48] and Nwe Gwe Hill in the north of Myanmar [49] (two dark orange dots in Fig. 1). At the same time, at least dozens of Neanderthal sites have been excavated – as examples in Europe in Fig. 1, well-known caves of Goyet [50, 51], Vindija [52] and Klissoura [53] are marked with dark orange dots. They are located in the space from North-Western Europe to Southern Greece, and these are just examples, so in Fig. 1 it is simply impossible to display the number of Neanderthal sites in Europe, and especially in Levant, in any way corresponding to reality. And in Asia, the areas of Neanderthals and Denisovans closed up at least from time to time. And everywhere there could be contacts between our ancestors and Neanderthals.

The second paradox: obvious contacts presence of northerners with Denisovans – northeastern hominins, and the complete absence of their haplotypes in genome of our ancestors – northerners.

The third paradox, one might say the most egregious: two largest Y-haplogroups of modern Europeans, R1a and R1b, are descendants of haplogroup P. In aboriginal Philippine Aita population (about a dozen related tribes, overwhelmingly from Luzon), the basal haplogroup P* reaches 28 %, and there also subclades P1* (M45) and P2 (P-B253) were found. This is the only population where there is such a concentration of this haplogroup, maternal in relation to those two main haplogroups of modern Caucasians. Only Timor inhabitants can observe something more or less similar – the basal P* there gives a share of about 10 %. In addition, Luzon Island is the only place on the Earth where the P*, P1* and very rare P2 clades are found together [54]. At the same time, Aita population (Magbukun, Manide, Indi, Ambala, Lopez, and Antsi tribes) is the world record holder for Denisovan impurities in genome – Denisovans part reaches 4.5 % (with extrapolation to the complete exclusion of late East Asian impurities), which is 1.5 times more than the recent "record holders", Papuans of New Guinea, and 10 times more than the majority of Asians [55]. And at the same time, according to DNA genealogy data, most of Caucasian is the direct descendants on paternal line of population, from which Aita differ less than anyone else, does not have even traces of Denisovans genome, which is so noticeable in Aita.

It is impossible to explain the distribution of Neanderthal and Denisovan impurities in sapiens genome, which leads to three paradoxes described above, within the framework of any version of generally accepted paradigm of modern man genesis. At the first moment after formulation of these paradoxes, it also seemed to us that it would not be easy to consistently link all the facts described in this section into a single chain. However, an understanding soon arose that this connection had already arisen in the works [1 – 3], moreover, completely without any efforts directed towards this and, as it were, quite spontaneously. After some reflection, it became clear that network of 88 points built there according to archaeological data and presented in those works in the figure, evolvement of which is Fig. 1 of this article, after imposition of logistic, geological, paleoclimatic, physical and some other restrictions on it, which turned this network into a directed graph characterizing the processes that took place with our ancestors in the period 130 – 30 ka BP, resolves all these contradictions elementarily.

In course of a more detailed consideration of these "genomic paradoxes", as well as problems discussed further in Section VI, 20 points were added to these 88 points – these are the above-mentioned Boker Tachtit, Denisova and Baishiya caves (both by two points – as the caves of Denisovans and as the caves of sapiens), Quesang and Nwe Gwe Hill, the Neanderthal Goyet (which also later became sapiens), Vindia and Klissoura. In addition, sites of sapiens: Kara-Bom in Altai, Shuidungou in China and Salkhit in Mongolia, Zlatý Kůň in Czechia, Nwya Devu in Tibet, Badahlin in Myanmar, and again Lao cave Tam Pa Ling, were considered, since an early, pre-catastrophic settling, and Duoi U'Oi Cave in North Vietnam. Also 2 stone tool workshops located nearby in Lenggong Valley on modern Malacca Peninsula were considered – before catastrophic Bukit Bunuh and after catastrophic Kota Tampan, see below. As a result, 108 points are shown in Fig. 1. And everything that at the first glance seemed insoluble paradoxes has now become only an additional confirmation of correctness of modern mankind genesis concept proposed in the works [1 – 3].

Indeed, the resolution of the first paradox is as follows: after the first contacts with Neanderthals in Zagros or Iranian Highlands, emigrants from Africa, who had not yet been divided into separate populations (not counting the disappeared Levantine Sapiens), they received a certain share of Neanderthal genes and passed on to them theirs. According to analysis of Altai Neanderthal genome, this happened about 100 ka BP [36], which is completely consistent with the time of sapiens movement eastward across Asia after their departure from the north of Arabia about 120 ka BP before the arrival in India of 96 – 95 ka BP. After that, the ancestors of easterners and southerners moved further to the east and southeast and never again encountered Neanderthals. The population of sapiens, which seized the enclave in Levant, actively interacted with local Neanderthals, but after the Catastrophe it completely died no later than 70 ka BP, and simply could not pass on its Neanderthal impurities in genome to descendants [1 – 3].

An attentive reader may, by the way, notice that in the previous paragraph, within the framework of generally accepted paradigm of modern mankind genesis, a new, fourth paradox almost spontaneously arose: the exit of sapiens from Africa was supposedly 60 – 50 ka BP, even 70, and their genes fell to Neanderthal, whose descendants went to Altai, "about 100 ka BP". But within the framework of the proposed concept, of course, there is no paradox here.

Even before the Catastrophe, sapiens that remained in North India, in search of water in drying steppe/semi-desert, went north to glacier in foothills of Pamir in Khatlon and became Cro-Magnon northerners. Starting thence a new resettlement from Asian central position in all directions, by the time of ~ 55 ka BP, they again collided in Levant with Neanderthals living there, having unleashed a new military campaign against them. And then something happened that determined all further relations of northerners with hominins of all other species. The Levantine campaign suddenly went so that it can be described by slogans in modern language: "Don't take captives" and "Don't surrender alive". Who was the first to start this war for total destruction of enemy is unclear. Either northerners, 15 – 17 kyr after death of brothers of their ancestors, found material traces of sapiens genocide carried out by Neanderthals after the Catastrophe, or Neanderthals, if by that time they had already appeared rudiments of magical thinking, perceived the newly arrived strangers as dead men destroyed by their ancestors but who rose from underground, and who must be killed again without exception, otherwise there will never be peace from them. One way or another, it happened.

Another unusual feature of this military campaign, which clearly manifested itself later in European War, was that two populations of northerners fought there, which the famous Soviet anthropologist G. F. Debets recon to "Pleistocene races", Brno-Předmosti and Grimaldi [1]. Typically, the dispersal of species is well described by the diffuse model [56], but it necessarily involves a gradual divergence of population, and no two "races", or rather, two populations in one place at the same time, according to this model. Nevertheless, war for a small region of Levant near the Mediterranean coast lasted for about 7.5 kyr, and the subsequent conquest by the same Cro-Magnon sapiens populations of all large periglacial Europe, which followed, required 4 kyr only [1 – 3]. Apparently, the only possible option explaining all these features of hostilities conduct at that time was presented in [1]: future Grimaldi were the first to come to Levant and start the war. Immediately after the war became total, they turned for help to their homeland, to Pamir Khatlon, and those whom anthropologists later began to call "Brno-Předmosti race" or "Brünners" briefly, who arrived in time by the end of Levantine campaign and define its quick completion (introduction of reserves at a critical moment in the development of operation is ABC of military strategy).

Typical rate of Cro-Magnon-northerners expansion at that time was about 0.5 km/year; after several thousand years, rate in Europe invasion was about 0.93 km/year [1 – 3]. If Brünners moved to Levant with an intermediate speed of ~ 0.7 km/year, then to overcome the distance along the paths of pedestrian crossings of about 4350 km they would need about 6 kyr. So the time of order of 0.5 kyr or less to get information about the genocide in Levant and to call for help for small forward detachment, and to participate in final victorious phase of the war at least 1 – 1.5 kyr, should have been enough for them. All northerners from Pamir were supposed to learn ~ 54 ka BP of news about what was happening in Levant. And when, soon after that, they began to populate periglacial mammoth steppe [1 – 3], and in the northeast they, never seen Neanderthals, encountered Denisovans, they could not to distinguish these two species and transferred their sharply negative attitude towards Neanderthals on these hominins. This is evidenced by data from the Altai Denisova Cave (a pair of dark orange and black dots in Fig. 1) [18] and Kara-Bom site (black dot next to each other) [57], and Chinese Baishiya Cave [47] (the same pair of dots, like at Denisov's Cave), and Shuidungou site [22] (yellow dot that is slightly northeast).

So we can assume that after these events Neanderthal and Denisovan "impurities" in any noticeable quantities never again entered the genome of northerners. Separate incidents, apparently, did occur. In Europe, in Bulgarian, Romanian, and Czech caves Bacho Kiro, cu Oase and Zlatý Kůň, fragments of DNA with noticeable Neanderthal impurities were extracted from remains of Cro-Magnons [58 – 60]. These finds refer to first appearance of Cro-Magnons in Eastern and Central Europe – to period 45 – 43 ka BP. However, in remains from Bacho Kiro and Zlatý Kůň caves, share of Neanderthal admixtures to the genome was only 3 – 3.8 %, which is less than the share of Denisovan admixtures even in modern Magbukun tribe from Aita people – up to 4.5 % [55], and in general it is comparable with the maximum rates for modern humans – 2 % [31], so it could well be a trace of early contact of Cro-Magnon ancestors with Neanderthals in the Middle East about 100 ka BP [36]. Only in cu Oase Cave, Neanderthal lobes in genome of remains of two people are more significant – 6 and 10 %. That is, apparently, at least womenfolk of enemy were still sometimes left alive by one of the opposing sides. But the consequences of these incidents, noticeable by modern genetic methods, have not been found to this day – the genome of Caucasians, like all other modern humans, has only one Middle Eastern Neanderthal admixture (from Zagros or its eastern environs) [42]. Perhaps this was due to the fact that carriers of these impurities, if they still existed 4 – 6 kyr later, died in all-European catastrophe caused by explosion of Archiflegreo volcano [60]. Thus, following the fourth, the second paradox is also resolved here. Let's move on to the other two.

On the contrary, easterners, southerners and their common ancestors, apparently, have never been subjected to genocide by any hominins, and, therefore, were much more tolerant of them than northerners did. In genomes of easterners and southerners descendants (Mongoloids and Melanoids), two lineages of Denisovan haplotypes were found for every race, and there are 3 of them in total [13, 27, 42, 45], despite the fact that, according to modern concepts, Denisovans were a very small species, and contacts with first, undivided pre-catastrophic sapiens, and then easterners, should have had a little of them. The southerners generally went to Sahul and completely isolated themselves there for many tens of thousands years.

Comparing possible, but quite obvious in some permissible limits, the paths of movement of pre-catastrophic sapiens in India and Southeast Asia [1 – 3] with probable location of Denisovans in southern Asia near Tibetan glacier and in mountains of Indochina, the closest to Tibet, but not on the path of easterners' ancestors, who came to the east of Sunda in the area of modern Palawan Island, we get very probable conclusions that D2 line genes were captured by sapiens somewhere on the southern approaches to Tibet about 95 – 85 ka BP, and genes of D1 line by ancestors of southerners only in sporadic contact with a small group of Denisovans a little later, somewhere not too far from Rakhine Mountains in modern western Myanmar or on Shan Plateau, lying a little to the east. These mountains have the same maximum height as mountains of Lebanon, the surroundings of which were chosen by Levantine Neanderthals, as well as these mountains are located next to the sea coast and lie only 12° – 13° south of Lebanon, but almost adjoined the giant Tibetan glacier at that time. And on Shan Plateau, with an average height of at least 1 km, where in British colonial times white administration of Mandalay escaped from heat of Burmese summer [61], it turned out that there are many Pleistocene sites, unfortunately dated slightly better than nothing [49].

It is worth that 10 days after these lines were written about Denisovans who found themselves "somewhere on the southern approaches to Tibet" an article was published about handprints of hominins left about 200 ka BP in the southern part of Tibet not far from Quesang in warm springs at altitude of about 4.3 km (dark orange point in Fig. 1). And it is very likely that these were Denisovans "from the southern approaches to Tibet" who visited this "high-mountainous thermal resort" [48]. By the way, this is quite correlated with separation time of the southwestern Denisovan (line D2) from the northern 285 ka BP. Sapiens settled in those places much later, 40 – 30 ka BP at the high-mountain lakeside site Nwya Devu (yellow dot with a green center next to the orange one in Fig. 1) [62]. In addition, two weeks later, after a targeted search for archaeological sites in Myanmar, author of this work became aware of the Middle Pleistocene site Nwe Gwe Hill between Rakhine Mountains and Shan Plateau, discovered about 40 years ago (dark orange point in Fig. 1 to the south-east of Quesang) and supposedly also originated about 200 ka BP, at about the same time when the alleged Denisovans appeared in Quesang. And approximately simultaneously with the sapiens site in Tibet, no later than 30 ka BP, the same site appears on the Shan Plateau in Badahlin Cave [49] (another yellow dot with a green center in Indochina in Fig. 1).

Considering a newly emerging information that in famous Tam Pa Ling Cave of sapiens, located in northern Laos (a pair of light green and blue dots in Fig. 1), along with post-catastrophic layers (see [1 – 3]) was excavated a layer with an age of 70 ± 8 ka BP [63], which can be attributed to pre-catastrophic time ("about 20 kyr older" than the previously found layers with fossils), the path along which the ancestors of easterners came out quite clearly – from northern India along Tibet, bypassing Rakhine Mountains and Shan Plateau from the north, to the east coast of Sunda and further southeast to Palawan Iceland. At the same time, resettlement also took place to the north, and it seems that North Vietnamese Duoi U'Oi Cave, located somewhat northeast of Laotian Tam Pa Ling (blue-green dot with a dark orange center in Fig. 1), preserved traces of death of people and animals after the Catastrophe, because of volcanic ash. It is designated in this way, since it has not yet been possible to determine which hominin teeth (sapiens, Denisovans, or erectus) were found there [64]. And ancestors of southerners immediately from the foothills of Tibet had to go south past Rakhine Mountains approximately along the eastern coast of Sunda up to the southern end of this subcontinent. This is confirmed by disastrous sapiens workshop Kota Tampan, located in Lenggong Valley near the western coast of Malacca Peninsula (green dot from a pair with black near Toba volcano in Fig. 1; black dot – a similar stone workshop Bukit Bunuh in the same valley, but 30 – 35 kyr later) [65].

An admixture of D0 line, which easterners passed on to inhabitants of East Asia, appeared later, about 45 – 40 ka BP, during expansion of easterners across Taiwan to the northwest. In Mongolia, in burial of Salkhit site (yellow dot with a green center), a very archaic woman with sapient mtDNA, but with a significant Denisovan admixture in the genome, was found in 35 – 34 ka BP age. Her Denisovan ancestors lived at least 6 kyr before her birth [66, 67].

Probably, there were other populations of Denisovans in Southeast Asia, possibly transferring their genes to sapiens settling there, but all of them and/or all of their descendants died in the Catastrophe and left their genetic trace nowhere. Consequently, the first paradox received its resolution here by this moment.

Well, and finally, consider the problem of Caucasians with haplogroups R1a and R1b and their direct ancestors on the paternal line, from which Filipino Aita differ less on Y-chromosome than anyone else on the planet. In accordance with the proposed concept, the ancestors of easterners received admixtures of Denisovan D2 line somewhere south of Tibet, survived the Catastrophe of 72 ka BP on Palawan Island and reached Luzon refugium by 67 ka BP, from where, after ~ 20 kyr, easterners began to settle through Taiwan peninsula in the times of the Ice Age across expanses of East Asia, becoming Mongoloids. And here they received Denisovan D0 line, and then began to intensively mix with Eastern Caucasians, at the same time displacing them from East and Southeast Asia. As a rule, Neanderthal and Denisovan alleles negatively affect the viability of sapiens, and over time they are washed out of the genotype [42]. The larger the populations were, the more intensively Mongoloids crossed with Caucasians, the faster elimination of Denisovan alleles, including those that entered the genomes of mestizos with mainly Caucasian morphology, took place. Indeed, it follows from Fisher's fundamental theorem of natural selection that the rate of evolution by selection is proportional to the effective size of population [68, 69].

And in genes of carriers of "Asian" Y-haplogroups R1a and R1b – the "new Caucasians", which largely replaced inhabitants of Old Europe and settled in America and Australia in New Age, Denisovan admixtures remained in quantities that were not detected by the methods of modern paleogenetics, if stayed at all. And the direct descendants of easterners – Aita continued to live on Luzon Island in isolation in their mountains and jungle for tens of thousands years, and the effective size of their local populations was negligible compared to what it was in "big world" (now, taking into account the fragmentation of Aita for individual tribes, it is no more than 10^{-5} of the effective size of the Caucasian populations [70]). Aita rarely came into contact with outside world, and, thus, conserved their genome as much as possible, preserving in it clear traces of Denisovans D2 line genes. Moreover, in small populations, genetic drift plays a decisive role, with the help of which neutral and even harmful, but not lethal, mutations are often fixed randomly, while in large populations even a weak negative effect will be enough to eliminate the corresponding allele [68].

So, the resolution of the third paradox is obvious, however, only on condition of recognition that Luzon Island was a refugium for the ancestors of Asians.

VI. Influence of cross breeding on the genesis of Neanderthals and modern man

In conclusion, one should return to Denisova 11 "mestizo girl" from Altai cave, which was mentioned in interview with A. P. Derevianko (November 2018) [19]. Both an earlier report by the institute where he works

(August 2018, see [71]) and a later one (December 2019, see [72]), it is reported that she was not a great-granddaughter, but daughter of a pair of Denisovan father and Neanderthal mother, which is a much more interesting and extremely important case of direct fixation of two human species crossing. The same is stated in the article in Nature [73], in which the academician is co-author. How the daughter in his interview was able to turn into a great-granddaughter, "thus finally confirming" "the possibility of the hypothesis that a modern human being was formed from four ... subspecies", we are not able to understand.

It is important that this child was a girl. Haldane's rule states: "If in offspring of interspecific hybrids one of the sexes is less common, completely absent or sterile, then this sex is usually heterogametic" [68]. In mammals, the heterogametic sex (with different sex chromosomes X and Y) is known to be male. Therefore, from the fact of birth of a girl in a Neanderthal-Denisovan pair, it does not follow at all that such pairs may bear of boys. The most recent studies are in agreement with this statement: in cases where Neanderthal mothers carried children from sapiens and Denisovans, hemolytic diseases of the fetus and newborn could occur due to the incompatibility of blood of fetus and mother according to Rh-factor [44, 74]. After all, the Altai mixed girl died early – at the age of 13.

There has been, however, an attempt to identify the so-called "Mezzena jaw" as a result of crossbreeding with a sapiens father and a Neanderthal mother [75], although this does not appear to have been convincing enough. The opposite situation with Neanderthal fathers and mothers from other human species seems to be completely (at least not yet) not visible, if we restrict to the exit horizon of modern man ancestors from Africa 130 ka BP.

However, earlier, with a much shorter time since the separation of considered species of hominins, everything could be completely different. Nuclear DNA analysis [76] shows that Neanderthals and Denisovans belong to sister groups that split from modern humans between 550 and 765 ka BP (this is the time from the last common Neanderthal-Denisovan and Sapient ancestor – TMRCA). More lately work (5 years after) [50] reduces this time to approximately 530 ± 30 ka BP. But the time before TMRCA for Neanderthals and modern humans, according to the results of sequencing of mitochondrial DNA (mtDNA), unexpectedly turned out to be much closer to the present – 470 – 360 ka BP [77] or 485 – 365 ka BP [50]. That is, on the maternal side, Neanderthals are closer to sapiens than to Denisovans. At the same time, it is known that in early Neanderthals, up to about 430 ka BP, their mtDNA did not show signs of sapiens, but were, as expected, related to Denisovans [78, 79]. Approximately the same, but with slightly less accuracy, turned out to be in Y-DNA analysis – the divergence of Neanderthals and ancestors of modern humans lines allegedly happened about 455 – 275 ka BP [80].

For physical and geographical reasons, an attempt to leave the ancestors of sapiens from Africa, after which they could have met Neanderthals, was possible in the range 420 – 395 ka BP, when both North African and Arabian deserts were relatively easy to overcome [1]. So, in accordance with the complex of all these data, the Neanderthal-Sapient crossing took place about 410 ± 15 ka BP, when their lines did not diverge too much (about 120 kyr passed after their separation according to the source [50]). Further, due to selection, early Neanderthals, who had genes in common with Denisovans, were ousted by mestizos, but no traces of sapiens who participated in that episode remained. At the same time, geographically isolated Eastern Neanderthals survived under the name of Denisovans. That is, lines of parents of Denisova 11 girl, who lived about 90 ka BP, were separated by about 320 kyr, so that the genomic compatibility of her parents, at least partial (with descendants of homogametic sex), was still possible. Approximately the same amount of time has passed since the transfer of genes from sapiens and Neanderthals to the time of 120 – 100 ka BP, when there was "the only serious episode of mixing" [42] in the time interval that we are considering 130 – 30 ka BP. At the same time, no traces of hybridization with sapiens were found in genomes of late European Neanderthals [50]. And from separation of sapiens and Denisovans lines to the moment of their contacts in Southeast Asia (90 – 80 ka BP), about 450 kyr passed, but, nevertheless, Denisovan admixtures were recorded in modern Mongoloids and Melanoids.

However, it should be remembered that size of populations, as a rule, grew approximately in inverse proportion to their distance in time from the present moment (see [1]), and in accordance with Fisher's theorem the rate of evolution by selection grew at the same rate. Therefore, one should expect an increase in the rate of evolution of hominins by an order of magnitude from the moment of Neanderthals appearance to the moment of their disappearance. Consequently, the closer to our time, the faster the divergence of hominin lines could reach points of partial or complete sexual incompatibility of species. And a noticeably longer (1.4 times) interval of time elapsed from separation of sapiens and Neanderthal-Denisovans ancestors to hybridization of sapiens and Denisovans in the vicinity of Tibet than interval between the separation of Neanderthals and Denisovans and their hybridization in Altai, in reality meant little, since the evolution speed at the moments of separation was 4 – 5 times lower than at the moments of hybridization.

As a result, we can say that the presence of Neanderthal and Denisovan alleles (in form of impurities) in modern human genome with the features that were described in the previous section of the article is confidently established, however, there is no evidence of any noticeable influence on its formation. In support of this thesis, it can be indicated that all lines of both Y-DNA and mtDNA haplogroups known to us date back to sapient African ancestors.

Conclusion

The work considers 7 paradoxes associated with the genesis of modern humanity. They are the following contradictions, insoluble within the framework of any version of modern description of this process:

- genetic monocentricity and cultural (artifact) polycentricity of the ancestors of modern mankind – northerners, southerners and easterners;
- one-time exit of sapiens from Africa according to genomics data, and their repeated appearance in a number of regions of Asia according to archaeological data;
- allegedly genomic incompatibility of Africans and non-Africans, and, at the same time, the presence of common haplogroups in them;
- a contradiction, consisting in a significant number of long-term and close contacts between Neanderthals and northerners, with a low diversity of Neanderthal haplotypes in their descendants, and a significantly greater diversity of Denisovan haplotypes in genome of southerners and easterners descendants with a relatively small number of sporadic contacts of their ancestors with Denisovans;
- clear presence of contacts between northerners and Denisovans – northeastern hominins after the Catastrophe, and complete absence of their haplotypes in genome of Caucasians – descendants of northerners;
- complete absence of Denisovan haplotypes in genome of Caucasian mestizos – carriers of Y-haplogroups R1a and R1b despite the fact that for the closest relatives of their paternal ancestors – Filipino Aita, Denisovan impurities in the genome are maximum among all currently known populations on the Earth;
- appearance of sapiens impurities in Neanderthals genome about 100 ka BP, which is impossible when sapiens leave Africa not earlier than 70 – 50 ka BP.

It is shown that all the above-described features of modern mankind genesis, manifested as insoluble paradoxes within the framework of the previous paradigm, become not only a natural consequence of this process in accordance with the concept described in [1 – 3], but also additional evidence that it is and so it happened. Thus, within the framework of the proposed paradigm, all problems, contradictions and paradoxes associated with the genesis of modern humanity, even those of an old nature, are easily resolved. At the same time, there is no evidence of any noticeable influence on modern mankind genesis of his cross-breeding with other species of hominins.

Literature

1. Yu. I. Lobanovsky – Great War and three ancestral homelands of modern humans. *Synerjetics Group*, 15 April 2021, 72 p. // http://www.synerjetics.ru/article/3_ancestral_lands.pdf (in Russian)
2. Yu. I. Lobanovsky – Origin of modern humanity in the light of system analysis. Synerjetics Group, 30 April 2021, 18 p. // http://www.synerjetics.ru/article/3_ancestral_homelands.pdf (in Russian)
3. Yu. I. Lobanovsky – Origin of modern humanity in the light of system analysis. *South Florida Journal of Development*, **2**(3), 26 July 2021, pp. 1 – 29 // https://southfloridapublishing.com/ojs/index.php/jdev/article/view/595
4. J. G. Fleagle et al. – Palaeoanthropology of the Kibish Formation, southern Ethiopia: Introduction. *Journal of Human Evolution*, **55**, September 2008, pp. 360 – 365 // https://www.sciencedirect.com/science/article/abs/pii/S0047248408000985
5. S. P. McPherron et al. – The age of the hominin fossils from Jebel Irhoud, Morocco, and the origins of the Middle Stone Age. *Nature*, **546**, 8 June 2017, pp. 293 – 296 // https://www.nature.com/articles/nature22335
6. A. P. Derevianko and M. V. Shunkov – How many ancestors does a modern m human have? In Defence of Science, no 9, 2011 // https://studylib.ru/doc/2069162/skol._ko-predkov-u-sovremennogo-cheloveka%3F (in Russian)
7. N. F. Nesturkh – Origin of human. Moscow, Nauka, 1970, 440 p. (in Russian)
8. E. P. Friedman – Primates. Moscow, Nauka, 1979, 208 p. (in Russian)
9. V. A. Ostapenko – The case of hybridization of rhesus monkey and hamadryas, in: Questions of applied primatology. Moscow, Moscow Zoo, 2004, pp. 112 – 115 // https://moscowzoo.ru/upload/iblock/739/739cc9b1a5a4f09049119f35eedf7ac5.pdf (in Russian)
10. A. Bowcock et al. – High Resolution of human evolutionary Trees with polymorphic microsatellites. *Nature*, **368**(6470), April 1994 // https://www.researchgate.net/publication/15687958_High_Resolution_of_human_evolutionary_Trees_with_polymorphic_microsatellites
11. Y-DNA Haplogroup Tree 2018 // https://isogg.org/tree/ISOGG_YDNATreeTrunk.html
12. A. Scally and R. Durbin – Revising the human mutation rate: implications for understanding human evolution. *Nature Reviews*, **13**, 11 September 2012, pp. 745 – 753 // https://www.nature.com/articles/nrg3295

13. J. C. Teixeira et al. – Widespread Denisovan ancestry in Island Southeast Asia but no evidence of substantial super-archaic hominin admixture. *Nature Ecology & Evolution*, **5**, 22 March 2021, pp.616 – 624 // https://www.nature.com/articles/s41559-021-01408-0
14. S. Pääbo et al. – The complete genome sequence of a Neanderthal from the Altai Mountains. *Nature*, **505**, 2014, pp. 43 – 49 // https://www.nature.com/articles/nature12886
15. D. Reich et al. – The genomic landscape of Neanderthal ancestry in present-day humans. *Nature*, **507**, 2014, pp. 354 – 357 // https://www.nature.com/articles/nature12961
16. A. Markov – There was a partial reproductive isolation between sapiens and Neanderthals. Elements, Science News, 03 February 2014 // https://elementy.ru/novosti_nauki/432184/Mezhdu_sapiensami_i_neandertaltsami_sushchestvovala_chastichnaya_reproduktivnaya_izolyatsiya (in Russian)
17. A. P. Derevianko – Upper Paleolithic in Africa and Eurasia and formation of a human of modern anatomical type. Novosibirsk, Publishing House of the Institute of Archeology and Ethnography of Siberian Branch of Russian Academy of Sciences, 2011, 561 p. // https://www.klex.ru/s6d (in Russian)
18. A. P. Derevianko et al. – Who are the Denisovans? *Archeology, Ethnography and Anthropology of Eurasia*, 48, no 3, 2020. (in Russian)
19. The Denisovan genome confirmed the Siberian scientist's hypothesis about ancestors of modern human. *TASS*, Novosibirsk, 09 November 2018 // https://tass.ru/sibir-news/5774220 (in Russian)
20. D. S. Brose and M. H. Wolpoff – Early Upper Paleolithic Man and Late Middle Paleolithic Tools, *American Anthropologist*, **73**(5), 1971, pp. 1156 – 1194 // https://www.researchgate.net/publication/227611808_Early_Upper_Paleolithic_Man_and_Late_Middle_Paleolithic_Tools
21. L. B. Vishnyatsky – Cultural dynamics in the middle of Late Pleistocene and causes of Upper Paleolithic revolution. St. Petersburg, St. Petersburg State University Publishing House, 2008 // http://www.archeo.ru/izdaniya-1/vagnejshije-izdanija/izdaniya-po-godam/pdf/Vishnjatskij_2008.PDF (in Russian)
22. A. N. Chekha – History of Shuidungou Paleolithic site study. *Humanities in Siberia*, no 2, 2013 // https://www.sibran.ru/upload/iblock/aa9/aa9e9d7d89930b2d409dcf904f4a332c.pdf (in Russian)
23. P. Škrdla – Bohunice in Moravia territories and neighboring regions. *Archaeologists, ethnography and anthropology*, no 3 (55), July – September 2013, pp. 2 – 13 // https://journal.archaeology.nsc.ru/jour/article/view/28/29 (in Russian)
24. A. J. Toynbee – A Study of History. London, Oxford University Press, Thames and Hudson, 1972, 576 p.
25. A. Markov – A new confirmation of sapiens early exit from Africa by "southern route" was found. *Elements, Science News*, 02 February 2011 // https://elementy.ru/novosti_nauki/431505/Naydeno_novoe_podtverzhdenie_rannego_vykhoda_sapiensov_iz_Afriki_yuzhnym_putem (in Russian)
26. S. J. Armitage et al. – The Southern Route "Out of Africa": Evidence for an Early Expansion of Modern Humans into Arabia. *Science*, **331**, 6016, 28 January 2011, pp. 453 – 456 // http://science.sciencemag.org/content/331/6016/453.full
27. A.-S. Malaspinas et al. – A genomic history of Aboriginal Australia. *Nature*, **538**, 21 September 2016, pp. 207 – 214 // https://www.nature.com/articles/nature18299
28. A. Markov – New genomic data have made it possible to clarify history of settlement of Eurasia and Australia. *Elements, Science News*, 28 September 2016 // https://elementy.ru/novosti_nauki/432841/Novye_genomnye_dannye_pozvolili_utochnit_istoriyu_zaseleniya_Evrazii_i_Avstralii (in Russian)
29. C. J. Bae et al. – On the origin of modern humans: Asian perspectives. *Science*, **358**, 6368, 8 December 2017 // http://science.sciencemag.org/content/358/6368/eaai9067
30. A. Markov – Data of archeology and genetics testify to the repeated attempts of African sapiens to populate Eurasia. *Elements, Science News*, 12 December 2017 // https://elementy.ru/novosti_nauki/433164/Dannye_arkheologii_i_genetiki_svidetelstvuyut_o_mnogokratnykh_popytkakh_afrikanskikh_sapiensov_zaselit_Evraziyu (in Russian)
31. Lu Chen et al. – Identifying and Interpreting Apparent Neanderthal Ancestry in African Individuals. *Cell*, **180**, Issue 4, 20 February 2020 , pp. 677 – 687 // https://www.sciencedirect.com/science/article/pii/S0092867420300593
32. A. Bergström et al. – Origins of modern human ancestry. *Nature*, **590**, 10 February 2021, pp. 229 – 237 // https://www.nature.com/articles/s41586-021-03244-5
33. A. Markov – Origin of mankind in the light of paleoanthropology and genetics new data. *Elements, Science News*, 15 February 2021 // https://elementy.ru/novosti_nauki/433769/Proiskhozhdenie_chelovechestva_v_svete_novykh_dannykh_paleoantropologii_i_genetiki2021, (in Russian)

34. M. Stewart et al. – Human footprints provide snapshot of last interglacial ecology in the Arabian interior. *Science Advances*, **6**, no. 38, 18 September 2020 // https://advances.sciencemag.org/content/6/38/eaba8940
35. Historical Temperatures. *Use Due Diligence on… Climate*, 2020 // https://www.use-due-diligence-on-climate.org/home/climate-change/temperatures/historical-temperatures/
36. M. Kuhlwilm et al. – Ancient gene flow from early modern humans into Eastern Neanderthals. *Nature*, **530**, 7591, 17 February 2016, pp. 429 – 433 // https://www.nature.com/articles/nature16544
37. Neanderthals mated with modern humans much earlier than previously thought. *Phis.org*, *Cold Spring Harbor Laboratory*, 17 February 2016 // https://phys.org/news/2016-02-neanderthals-modern-humans-earlier-previously.html
38. J. E. Huffman et al. – Multi-ancestry fine mapping implicates OAS1 splicing in risk of severe COVID-19. *Nature Genetics*, 13 January 2022 // https://www.nature.com/articles/s41588-021-00996-8
39. S. Pääbo et al. – A Draft Sequence of the Neandertal Genome. *Science*, **328**, 5979, 7 May 2010, pp. 710 – 722 // https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5100745/
40. A. Anderson – Neandertal Genome Points to Human-Neandertal Interbreeding. *GenomeWeb News*, **7** May 2010 // https://www.genomeweb.com/sequencing/neandertal-genome-points-human-neandertal-interbreeding#.YSvjLY4za00
41. G. D. Posnik et al. – Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. *Nature Genetics*, **48**, 25 April 2016, pp. 593 – 599 // https://www.nature.com/articles/ng.3559
42. A. Bergström et al. – Insights into human genetic variation and population history from 929 diverse genomes – *Science*, **367**, 6484, 20 March 2020 // https://science.sciencemag.org/content/367/6484/eaay5012
43. E. Boaretto et al. – The absolute chronology of Boker Tachtit (Israel) and implications for the Middle to Upper Paleolithic transition in the Levant. *PNAS*, **118**(25), 22 June 2021 // https://www.pnas.org/content/118/25/e2014657118.short
44. S. Condemi et al. – Blood groups of Neandertals and Denisova decrypted. *PLOS ONE*, 28 July 2021 // https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0254175
45. M. P. Cox – Multiple Deeply Divergent Denisovan Ancestries in Papuans. *Cell*, **177**, Issue 4, 10 April 2019, pp. 1010 – 1021 // https://www.cell.com/cell/fulltext/S0092-8674(19)30218-1.pdf
46. D. Reich et al. – Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature*, 468, 22 December 2010, pp. 1053 – 1060 // https://www.nature.com/articles/nature09710
47. Dongju Zhang et al. – Denisovan DNA in Late Pleistocene sediments from Baishiya Karst Cave on the Tibetan Plateau. *Science*, **370**, 6516, 30 October 2020, pp. 584 – 587 // http://science.sciencemag.org/content/370/6516/584
48. D. D. Zhang et al. – Earliest parietal art: hominin hand and foot traces from the middle Pleistocene of Tibet. *Science Bulletin*, 10 September 2021 // https://www.sciencedirect.com/science/article/pii/S2095927321006174
49. Tin Htut Aung et al. – Paleolithic Zooarchaeology in Myanmar. A Review and Future Prospects. *Journal of Indo-Pacific Archaeology*, **39**, 2015, pp. 50 – 56 // https://www.researchgate.net/publication/283220445_Palaeolithic_Zooarchaeology_in_Myanmar_A_Review_and_Future_Prospects
50. M. Hajdinjak et al. – Reconstructing the genetic history of late Neanderthals. *Nature*, **555**, 21 March 2018, pp. 652 – 656 // https://www.nature.com/articles/nature26151
51. H. Rougier et al. – Neanderthal cannibalism and Neanderthal bones used as tools in Northern Europe. *Scientific Reports*, 6 July 2016 // https://www.nature.com/articles/srep29005
52. T. Devièse et al. – Direct dating of Neanderthal remains from the site of Vindija Cave and implications for the Middle to Upper Paleolithic transition. *PNAS*, **114**(40), 3 October 2017, pp. 10606 – 10611 // https://www.pnas.org/content/114/40/10606
53. M. C. Stiner et al. – Klissoura Cave 1 and the Upper Paleolithic of Southern Greece in Cultural and Ecological Contexts. *Eurasian Prehistory*, 7(2), January 2010 // https://www.researchgate.net/publication/235767305_Klissoura_Cave_1_and_the_Upper_Paleolithic_of_Southern_Greece_in_Cultural_and_Ecological_Contexts
54. E. Heyer et al. – Genetic diversity of four Filipino negrito populations from Luzon: comparison of male and female effective population sizes and differential integration of immigrants into Aeta and Agta communities. *Human Biology*, **85**(1 – 3), Feb-Jun 2013, pp. 189 – 208 // https://pubmed.ncbi.nlm.nih.gov/24297226/
55. M. Larena et al. – Philippine Ayta possess the highest level of Denisovan ancestry in the world. *Current Biology*, **31**(19), 12 August 2021, pp. 4219 – 4230 // https://www.cell.com/current-biology/fulltext/S0960-9822(21)00977-5
56. A. Timmermann – Quantifying the potential causes of Neanderthal extinction: Abrupt climate change versus competition and interbreeding. *Quaternary Science Reviews*, 238, 15 June 2020 // https://www.sciencedirect.com/science/article/pii/S0277379120302936

57. N. E. Belousova and E. P. Rybin – A new scheme of cultural-stratigraphic division of Early Upper Paleolithic deposits of Kara-Bom site (based on spatial analysis and re-assemblage data). *Bulletin of NSU, History, Philology*, **12**(7), 2013, pp. 64 – 76 // https://vestnik.nsu.ru/historyphilology/files/7ad7acba885560f4e6fc4ced003066ef.pdf (in Russian)
58. M. Hajdinjak et al. – Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. *Nature*, **592**, 07 April 2021, pp. 253 – 257 // https://www.nature.com/articles/s41586-021-03335-3
59. J. N. Wilford – Fossil Teeth Put Humans in Europe Earlier Than Thought. *The New York Times, Science*, 2 November 2011 // https://www.nbcnews.com/science/science-news/tooth-offers-evidence-modern-humans-reached-europe-earlier-previously-thought-n1204401
60. K. Prüfer et al. – A genome sequence from a modern human skull over 45,000 years old from Zlatý kůň in Czechia. *Nature Ecology & Evolution*, **5**, 07 April 2021, pp. 820 – 825 // https://www.nature.com/articles/s41559-021-01443-x
61. Climate of Myanmar. *Britannica* // https://www.britannica.com/place/Myanmar/Languages
62. X. L. Zhang et al. – The earliest human occupation of the high-altitude Tibetan Plateau 40 thousand to 30 thousand years ago. *Science*, **362**, 6418, 30 November 2018, pp. 1049 – 1051 // https://nplus1.ru/news/2018/11/29/Tibet-site
63. L. Shackelford – Additional evidence for early modern human morphological diversity in Southeast Asia at Tam Pa Ling, Laos, *Quaternary International*, **466**, Part A, 1 February 2018, pp. 93 – 106 // https://www.sciencedirect.com/science/article/abs/pii/S1040618215302731
64. A.-M. Bacon et al. – The Late Pleistocene Duoi U'Oi cave in northern Vietnam: palaeontology, sedimentology, taphonomy and palaeoenvironments. *Quaternary Science Reviews*, **27**, Issues 15 – 16, August 2008, pp. 1627 – 1654 // https://www.sciencedirect.com/science/article/abs/pii/S0277379108001145
65. Lenggong Valley (Malaysia). *UNESCO World Heritage Centre – World Heritage List*, No 1396, 2010 // https://whc.unesco.org/document/152564
66. S. Drobyshevsky – Is Salkhit a Denisovan or a Sapiens? *Anthropogenesis.RU*, 02 February 2019 // https://antropogenez.ru/single-news/article/761/ (in Russian)
67. D. Massilani et al. – Denisovan ancestry and population history of early East Asians. *Science*, **370**, 6516, 30 October 2020, pp. 579 – 583 // https://www.science.org/doi/abs/10.1126/science.abc1166
68. E. V. Kunin – The logic of the case. On the Nature and Origin of Biological Evolution. Moscow, Center-Polygraph Publishing House, 2014, 527 p. (in Russian)
69. R. A. Fisher – The Genetical Theory of Natural Selection. Oxford, Clarendon Press, 1930, 272 p.
70. 2010 Census of Population and Housing. Republic of the Philippines. National Statistics Office, Manila // https://psa.gov.ph/sites/default/files/PHIILIPPINES_FINAL%20PDF.pdf
71. Father is Denisovan, mother is Neanderthal. *News of Siberian Science*, IAET SB RAS, 22 August 2018 // https://archaeology.nsc.ru/otets-denisovets-mat-neandertalka/ (in Russian)
72. Through millennia, light of Denisovan girl smile has reached us. *News of Siberian Science*, IAET SB RAS, 23 December 2019 // http://www.sib-science.info/ru/institutes/cherez-tysyacheletiya-do-21122019 (in Russian)
73. V. Slon et al. – The genome of the offspring of a Neanderthal Mother and Denisovan father. *Nature*, **561**, 22 August 2018, pp. 113 – 116 // https://www.nature.com/articles/s41586-018-0455-x
74. B. Foster – Neanderthal and Denisovan blood groups deciphered – NovLink. *Packaging News Online*, 20 September 2021 // https://packagingnewsonline.com/neanderthal-and-denisovan-blood-groups-deciphered-novlink/
75. S. Condemi et al. – Possible Interbreeding in Late Italian Neanderthals? New Data from the Mezzena Jaw (Monti Lessini, Verona, Italy). *PLOS ONE*, **9**(1), 27 March 2013 // https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0059781
76. K. Prüfer et al. – The complete Genome Sequence of a Neanderthal from the Altai Mountains. *Nature*, **505**, 18 December 2013, pp. 43 – 49 // https://www.nature.com/articles/nature12886
77. C. Posth et al. – Deeply divergent archaic mitochondrial Genome provides lower Time Boundary for African Gene Flow into Neanderthals. *Nature Communications*, **8**, 16046, 04 July 2017 // https://www.nature.com/articles/ncomms16046
78. M. Meyer et al. – A mitochondrial Genome Sequence of a Hominin from Sima de los Huesos. *Nature*, **505**, pp. 403 – 406, 04 December 2013 // https://www.nature.com/articles/nature12788
79. M. Meyer et al. – Nuclear DNA Sequences from the Middle Pleistocene Sima de los Huesos hominins. *Nature*, **531**(735), March 2016, pp. 504 – 507 // https://www.nature.com/articles/nature17405
80. M. Petr et al. – The evolutionary history of Neanderthal and Denisovan Y chromosomes. *Science*, **369**, 6511, 25 September 2020, pp. 1653 – 1656 // https://www.science.org/doi/10.1126/science.abb6460

Moscow,
30.01.2022

Yu. I. Lobanovsky